NCBI   results of BLAST

BLASTN 2.1.3 [Apr-11-2001]

RID: 990123014-1507-5082

Query=
(2644 letters)

Database: nt
861,799 sequences; 3,247,139,289 total letters

If you have any problems or questions with the results of this search
please refer to the **BLAST FAQs**

Taxonomy reports

Distribution of 105 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments

Sequences producing significant alignments:	Score (bits)	E Value
gi|13562129|gb|AY028435.1| Homo sapiens adaptor protein kan...	3478	0.0
gi|8922556|ref|NM_018158.1| Homo sapiens hypothetical prote...	3470	0.0
gi|7022771|dbj|AK001486.1|AK001486 Homo sapiens cDNA FLJ106...	3470	0.0
gi|13636382|ref|XM_002333.3| Homo sapiens hypothetical prot...	1949	0.0

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gi|2661089|gb|AF035526.1|AF035526   Mus musculus kanadaptin m...  1340   0.0
gi|1029496|emb|Z58265.1|HS33F3R    H.sapiens CpG island DNA ge...  428   e-117
gi|11182219|emb|AL357559.16|AL357559  Human DNA sequence fro...    141   2e-30
gi|11181843|gb|AC017028.11|AC017028  Homo sapiens BAC clone ...     48   0.028
gi|14010785|gb|AC069543.4|AC069543   Homo sapiens chromosome ...    46   0.11
gi|10443437|emb|AL356421.10|AL356421  Human DNA sequence fro...     46   0.11
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Alignments

>gi|13562129|gb|AY028435.1| Homo sapiens adaptor protein kanadaptin mRNA, complete cds
          Length = 2949

 Score = 3478 bits (1754), Expect = 0.0
 Identities = 1758/1760 (99%)
 Strand = Plus / Plus


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Sbjct: 414  gttgaggatggctgacattctctctcagtcagagaccctggcgtcgcaagacctcagtgg 473


Query: 61   ggacttcaagaagccagctctgccggtgtccccagcggcgcggagtaaggccccggccag 120
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Sbjct: 474  ggacttcaagaagccagctctgccggtgtccccagcggcgcggagtaaggccccggccag 533


Query: 121  cagttcttcaaaccctgaggaggtacagaaggaagggcccactgcgttgcaggactccaa 180
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Sbjct: 534  cagttcttcaaaccctgaggaggtacagaaggaagggcccactgcgttgcaggactccaa 593


Query: 181  ttctggggagcccgacatccctcctcctcagccggactgcggtgattttaggagtctaca 240
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Query: 241  ggaggagcagtcgcgcccccacgacagcggtttcttcccctggcggtccagcccgggctcc 300
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Sbjct: 654  ggaggagcagtcgcgcccccccgacagcggtttcttcccctggcggtccagcccgggctcc 713


Query: 301  cccctaccaagagcctccatggggtggccctgccacagcccccctacagcttagagaccct 360
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Sbjct: 834  gaggctgtctggctgcgacgtgtgcctggagcacccttcggtgtctcggtaccacgcagt 893


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Query: 721   gaaggaattgcgcaagcagcagcaaatattgttggrgaagaagatgctaggagaagactc 780
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Sbjct: 1134  gaaggaattgcgcaagcagcagcaaatattgttggagaagaagatgctaggagaagactc 1193


Query: 781   agatgaagaagaggaaatggatacctctgaaaggaagataaatgctggtagccaagatga 840
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Query: 841   tgagatgggttgcacctggggaatgggagaagatgcagtagaggatgatgctgaagagaa 900
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Sbjct: 1254  tgagatgggttgcacctggggaatgggagaagatgcagtagaggatgatgctgaagagaa 1313


Query: 901   ccctattgtcttagagtttcagcaggaaagggaggcctttttatataaaggatcccaaaaa 960
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Query: 961   ggctctccaaggcttttttgaccgagaaggagaagaattagaatatgaatttgatgaaca 1020
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Sbjct: 1374  ggctctccaaggcttttttgaccgagaaggagaagaattagaatatgaatttgatgaaca 1433


Query: 1021  gggacatagcacttggctctgcagggtgagattacctgtggacgattcaactggaaaaca 1080
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Query: 1081  actggtggctgaggccattcactcaggaaagaaaaaagaagcaatgatccagtgctcatt 1140
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Sbjct: 1494  actggtggctgaggccattcactcaggaaagaaaaaagaagcaatgatccagtgctcatt 1553


Query: 1141  ggaagcttgtcggattcttgacactttgggattgcttcggcaggaagcagtatctcggaa 1200
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Sbjct: 1554  ggaagcttgtcggattcttgacactttgggattgcttcggcaggaagcagtatctcggaa 1613


Query: 1201  aaggaaagccaagaactgggaagatgaagactttttatgatagtgatgatgacacatttct 1260
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Query: 1621  gactacaggtgcagaaaacaaagctaaaaagcttacattgcctctatttggtgccatgaa  1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2034  gactacaggtgcagaaaacaaagctaaaaagcttacattgcctctatttggtgccatgaa  2093


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Sbjct: 2154  agaactccctccaactctaa  2173

 Score =  222 bits (112), Expect = 8e-55
 Identities = 112/112 (100%)
 Strand = Plus / Plus


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Sbjct: 2263  ctggaggatggaagcctcagtaggccacagccagagatagagccagaagcagcagtgcag  2322


Query: 1910  gaaatgaggcctcccacagatctcacacattttaaagaaacccaaacccatg  1961
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Sbjct: 2323  gaaatgaggcctcccacagatctcacacattttaaagaaacccaaacccatg  2374

>gi|8922556|ref|NM_018158.1| Homo sapiens hypothetical protein FLJ10624 (FLJ10624), mRNA
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 Identities = 1757/1760 (99%)
 Strand = Plus / Plus


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Sbjct:  498   ggacttcaagaagccagctctgccggtgtccccagcggcgcggagtaaggccccggccag   557


Query:  121   cagttcttcaaaccctgaggaggtacagaaggaagggcccactgcgttgcaggactccaa   180
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Sbjct:  558   cagttcttcaaaccctgaggaggtacagaaggaagggcccactgcgttgcaggactccaa   617


Query:  181   ttctggggagcccgacatccctcctcctcagccggactgcggtgattttaggagtctaca   240
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Query:  241   ggaggagcagtcgcgccccacgacagcggtttcttcccctggcggtccagcccgggctcc   300
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Sbjct:  678   ggaggagcagtcgcgccccacgacagcggtttcttcccctggcggtccagcccgggctcc   737


Query:  301   cccctaccaagagcctccatggggtggccctgccacagccccctacagcttagagaccct   360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  738   cccctaccaagagcctccatggggtggccctgccacagccccctacagcttagagaccct   797


Query:  361   gaagggcggcactatccttggcacccgtagcttgaaagggacgagttactgccttttcgg   420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  798   gaagggcggcactatccttggcacccgtagcttgaaagggacgagttactgccttttcgg   857


Query:  421   gaggctgtctggctgcgacgtgtgcctggagcacccttcggtgtctcggtaccacgcagt   480
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Sbjct:  858   gaggctgtctggctgcgacgtgtgcctggagcacccttcggtgtctcggtaccacgcagt   917


Query:  481   gctgcagcacagggcgtccggccctgacggagaatgcgacagcaacgggccgggcttcta   540
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Sbjct:  918   gctgcagcacagggcgtccggccctgacggagaatgcgacagcaacgggccgggcttcta   977


Query:  541   cctctacgatctgggaagcacccatggcacttttctcaacaaaactcgcatcccacctcg   600
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Sbjct:  1098  tatcctgcagggaccagaggaagaccgagaggcagaatccgagttaacagtaacacagtt   1157


Query:  721   gaaggaattgcgcaagcagcagcaaatattgttggrgaagaagatgctaggagaagactc   780
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Sbjct:  1158  gaaggaattgcgcaagcagcagcaaatattgttggagaagaagatgctaagagaagactc   1217


Query:  781   agatgaagaagaggaaatggatacctctgaaaggaagataaatgctggtagccaagatga   840
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Query: 961  ggctctccaaggctttttttgaccgagaaggagaagaattagaatatgaatttgatgaaca 1020
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Query: 1021 gggacatagcacttggctctgcagggtgagattacctgtggacgattcaactggaaaaca 1080
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Query: 1081 actggtggctgaggccattcactcaggaaagaaaaaagaagcaatgatccagtgctcatt 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1518 actggtggctgaggccattcactcaggaaagaaaaaagaagcaatgatccagtgctcatt 1577


Query: 1141 ggaagcttgtcggattcttgacactttgggattgcttcggcaggaagcagtatctcggaa 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1578 ggaagcttgtcggattcttgacactttgggattgcttcggcaggaagcagtatctcggaa 1637


Query: 1201 aaggaaagccaagaactgggaagatgaagactttttatgatagtgatgatgacacatttct 1260
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Query: 1261 tgataggactggcctgattgagaagaagcgtctgaacagaatgaagaaggctggcaagat 1320
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Query: 1321 tgatgagaagccagagacctttgaatcattggttgcaaaattaaatgatgctgaaaggga 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query: 1441 tcaggattctttagatgcgttcatgtcagaaatgaaatcaggcagtacattagatggtgt 1500
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Query: 1501 gtcccggaagaaacttcacctgagaacttttgaactgaggaaagaacaacagagacttaa 1560
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Query: 1561 agggttaataaaaattgtaaagccagcagagattccagaactaaaaaagactgaaactca 1620
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Sbjct: 1998 agggttaataaaaattgtaaagccagcagagattccagaactaaaaaagactgaaactca 2057


Query: 1621 gactacaggtgcagaaaacaaagctaaaaagcttacattgcctctatttggtgccatgaa 1680
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 Score =  222 bits (112), Expect = 8e-55
 Identities = 112/112 (100%)
 Strand = Plus / Plus


Query: 1850  ctggaggatggaagcctcagtaggccacagccagagatagagccagaagcagcagtgcag 1909
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Sbjct: 2287  ctggaggatggaagcctcagtaggccacagccagagatagagccagaagcagcagtgcag 2346


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Sbjct: 2347  gaaatgaggcctcccacagatctcacacattttaaagaaacccaaacccatg 2398


>gi|7022771|dbj|AK001486.1|AK001486 Homo sapiens cDNA FLJ10624 fis, clone NT2RP2005525, highly
            Mus musculus kanadaptin mRNA
          Length = 2954

 Score = 3470 bits (1750), Expect = 0.0
 Identities = 1757/1760 (99%)
 Strand = Plus / Plus


Query: 1     gttgaggatggctgacattctctctcagtcagagaccctggcgtcgcaagacctcagtgg 60
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Query: 61    ggacttcaagaagccagctctgccggtgtccccagcggcgcggagtaaggccccggccag 120
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Sbjct: 498   ggacttcaagaagccagctctgccggtgtccccagcggcgcggagtaaggccccggccag 557


Query: 121   cagttcttcaaaccctgaggaggtacagaaggaagggcccactgcgttgcaggactccaa 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 558   cagttcttcaaaccctgaggaggtacagaaggaagggcccactgcgttgcaggactccaa 617


Query: 181   ttctggggagcccgacatccctcctcctcagccggactgcggtgattttaggagtctaca 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 618   ttctggggagcccgacatccctcctcctcagccggactgcggtgattttaggagtctaca 677


Query: 241   ggaggagcagtcgcgcccccacgacagcggtttcttcccctggcggtccagcccgggctcc 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 678   ggaggagcagtcgcgcccccacgacagcggtttcttcccctggcggtccagcccgggctcc 737


Query: 301   cccctaccaagagcctccatggggtggccctgccacagccccctacagcttagagaccct 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 738   cccctaccaagagcctccatggggtggccctgccacagccccctacagcttagagaccct 797
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Query:  361   gaagggcggcactatccttggcacccgtagcttgaaagggacgagttactgccttttcgg  420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  798   gaagggcggcactatccttggcacccgtagcttgaaagggacgagttactgccttttcgg  857


Query:  421   gaggctgtctggctgcgacgtgtgcctggagcacccttcggtgtctcggtaccacgcagt  480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  858   gaggctgtctggctgcgacgtgtgcctggagcacccttcggtgtctcggtaccacgcagt  917


Query:  481   gctgcagcacagggcgtccggccctgacggagaatgcgacagcaacgggccgggcttcta  540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  918   gctgcagcacagggcgtccggccctgacggagaatgcgacagcaacgggccgggcttcta  977


Query:  541   cctctacgatctgggaagcacccatggcacttttctcaacaaaactcgcatcccacctcg  600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  978   cctctacgatctgggaagcacccatggcacttttctcaacaaaactcgcatcccacctcg  1037


Query:  601   cacctactgtcgagtccacgttgggcatgttgttcgctttggaggcagcacccggctctt  660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1038  cacctactgtcgagtccacgttgggcatgttgttcgctttggaggcagcacccggctctt  1097


Query:  661   tatcctgcagggaccagaggaagaccgagaggcagaatccgagttaacagtaacacagtt  720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1098  tatcctgcagggaccagaggaagaccgagaggcagaatccgagttaacagtaacacagtt  1157


Query:  721   gaaggaattgcgcaagcagcagcaaatattgttggrgaagaagatgctaggagaagactc  780
              |||||||||||||||||||||||||||||||||||| |||||||||||| ||||||||||
Sbjct:  1158  gaaggaattgcgcaagcagcagcaaatattgttggagaagaagatgctaagagaagactc  1217


Query:  781   agatgaagaagaggaaatggatacctctgaaaggaagataaatgctggtagccaagatga  840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1218  agatgaagaagaggaaatggatacctctgaaaggaagataaatgctggtagccaagatga  1277


Query:  841   tgagatggggttgcacctggggaatgggagaagatgcagtagaggatgatgctgaagagaa  900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1278  tgagatggggttgcacctggggaatgggagaagatgcagtagaggatgatgctgaagagaa  1337


Query:  901   ccctattgtcttagagtttcagcaggaaagggaggccttttatataaaggatcccaaaaa  960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1338  ccctattgtcttagagtttcagcaggaaagggaggccttttatataaaggatcccaaaaa  1397


Query:  961   ggctctccaaggctttttttgaccgagaaggagaagaattagaatatgaatttgatgaaca  1020
              ||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1398  ggttctccaaggctttttttgaccgagaaggagaagaattagaatatgaatttgatgaaca  1457


Query:  1021  gggacatagcacttggctctgcagggtgagattacctgtggacgattcaactggaaaaca  1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1458  gggacatagcacttggctctgcagggtgagattacctgtggacgattcaactggaaaaca  1517


Query:  1081  actggtggctgaggccattcactcaggaaagaaaaaagaagcaatgatccagtgctcatt  1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1518  actggtggctgaggccattcactcaggaaagaaaaaagaagcaatgatccagtgctcatt  1577
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Query:  1141  ggaagcttgtcggattcttgacactttgggattgcttcggcaggaagcagtatctcggaa  1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1578  ggaagcttgtcggattcttgacactttgggattgcttcggcaggaagcagtatctcggaa  1637


Query:  1201  aaggaaagccaagaactgggaagatgaagactttttatgatagtgatgatgacacatttct  1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1638  aaggaaagccaagaactgggaagatgaagactttttatgatagtgatgatgacacatttct  1697


Query:  1261  tgataggactggcctgattgagaagaagcgtctgaacagaatgaagaaggctggcaagat  1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1698  tgataggactggcctgattgagaagaagcgtctgaacagaatgaagaaggctggcaagat  1757


Query:  1321  tgatgagaagccagagacctttgaatcattggttgcaaaattaaatgatgctgaaaggga  1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1758  tgatgagaagccagagacctttgaatcattggttgcaaaattaaatgatgctgaaaggga  1817


Query:  1381  actttctgaaatttctgagagattgaaagcctcaagccaagttctatcagagtctccatc  1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1818  actttctgaaatttctgagagattgaaagcctcaagccaagttctatcagagtctccatc  1877


Query:  1441  tcaggattctttagatgcgttcatgtcagaaatgaaatcaggcagtacattagatggtgt  1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1878  tcaggattctttagatgcgttcatgtcagaaatgaaatcaggcagtacattagatggtgt  1937


Query:  1501  gtcccggaagaaacttcacctgagaactttttgaactgaggaaagaacaacagagacttaa  1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1938  gtcccggaagaaacttcacctgagaactttttgaactgaggaaagaacaacagagacttaa  1997


Query:  1561  agggttaataaaaattgtaaagccagcagagattccagaactaaaaaagactgaaactca  1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1998  agggttaataaaaattgtaaagccagcagagattccagaactaaaaaagactgaaactca  2057


Query:  1621  gactacaggtgcagaaaacaaagctaaaaagcttacattgcctctatttggtgccatgaa  1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  2058  gactacaggtgcagaaaacaaagctaaaaagcttacattgcctctatttggtgccatgaa  2117


Query:  1681  aggaggaagcaaattcaaattaaaaactggaacagtagggaagttaccccccaagcgtcc  1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  2118  aggaggaagcaaattcaaattaaaaactggaacagtagggaagttaccccccaagcgtcc  2177


Query:  1741  agaactccctccaactctaa  1760
              ||||||||||||||||||||
Sbjct:  2178  agaactccctccaactctaa  2197

 Score =  222 bits (112), Expect = 8e-55
 Identities = 112/112 (100%)
 Strand = Plus / Plus


Query:  1850  ctggaggatggaagcctcagtaggccacagccagagatagagccagaagcagcagtgcag  1909
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  2287  ctggaggatggaagcctcagtaggccacagccagagatagagccagaagcagcagtgcag  2346


Query:  1910  gaaatgaggcctcccacagatctcacacatttttaaagaaacccaaacccatg  1961
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                    |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2347  gaaatgaggcctcccacagatctcacacattttaaagaaacccaaacccatg  2398


>gi|13636382|ref|XM_002333.3|  Homo sapiens hypothetical protein FLJ10624 (FLJ10624), mRNA
            Length = 2949

 Score = 1949 bits (983), Expect = 0.0
 Identities = 990/991 (99%), Gaps = 1/991 (0%)
 Strand = Plus / Plus


Query: 770   ggagaagactcagatgaagaagaggaaatggatacctctgaaaggaagataaatgctggt  829
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1203  ggagaagactcagatgaagaagaggaaatggatacctctgaaaggaagataaatgctggt  1262


Query: 830   agccaagatgatgagatgggttgcacctggggaatgggagaagatgcagtagaggatgat  889
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1263  ag-caagatgatgagatgggttgcacctggggaatgggagaagatgcagtagaggatgat  1321


Query: 890   gctgaagagaaccctattgtcttagagtttcagcaggaaagggaggccttttatataaag  949
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1322  gctgaagagaaccctattgtcttagagtttcagcaggaaagggaggccttttatataaag  1381


Query: 950   gatcccaaaaaggctctccaaggctttttttgaccgagaaggagaagaattagaatatgaa  1009
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1382  gatcccaaaaaggctctccaaggctttttttgaccgagaaggagaagaattagaatatgaa  1441


Query: 1010  tttgatgaacagggacatagcacttggctctgcagggtgagattacctgtggacgattca  1069
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1442  tttgatgaacagggacatagcacttggctctgcagggtgagattacctgtggacgattca  1501


Query: 1070  actggaaaacaactggtggctgaggccattcactcaggaaagaaaaaagaagcaatgatc  1129
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1502  actggaaaacaactggtggctgaggccattcactcaggaaagaaaaaagaagcaatgatc  1561


Query: 1130  cagtgctcattggaagcttgtcggattcttgacactttgggattgcttcggcaggaagca  1189
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1562  cagtgctcattggaagcttgtcggattcttgacactttgggattgcttcggcaggaagca  1621


Query: 1190  gtatctcggaaaaggaaagccaagaactgggaagatgaagactttttatgatagtgatgat  1249
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1622  gtatctcggaaaaggaaagccaagaactgggaagatgaagactttttatgatagtgatgat  1681


Query: 1250  gacacatttcttgataggactggcctgattgagaagaagcgtctgaacagaatgaagaag  1309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1682  gacacatttcttgataggactggcctgattgagaagaagcgtctgaacagaatgaagaag  1741


Query: 1310  gctggcaagattgatgagaagccagagacctttgaatcattggttgcaaaattaaatgat  1369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1742  gctggcaagattgatgagaagccagagacctttgaatcattggttgcaaaattaaatgat  1801


Query: 1370  gctgaaagggaactttctgaaatttctgagagattgaaagcctcaagccaagttctatca  1429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1802  gctgaaagggaactttctgaaatttctgagagattgaaagcctcaagccaagttctatca  1861
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Query: 1430  gagtctccatctcaggattctttagatgcgttcatgtcagaaatgaaatcaggcagtaca  1489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1862  gagtctccatctcaggattctttagatgcgttcatgtcagaaatgaaatcaggcagtaca  1921


Query: 1490  ttagatggtgtgtcccggaagaaacttcacctgagaacttttgaactgaggaaagaacaa  1549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1922  ttagatggtgtgtcccggaagaaacttcacctgagaacttttgaactgaggaaagaacaa  1981


Query: 1550  cagagacttaaagggttaataaaaattgtaaagccagcagagattccagaactaaaaaag  1609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1982  cagagacttaaagggttaataaaaattgtaaagccagcagagattccagaactaaaaaag  2041


Query: 1610  actgaaactcagactacaggtgcagaaaacaaagctaaaaagcttacattgcctctattt  1669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2042  actgaaactcagactacaggtgcagaaaacaaagctaaaaagcttacattgcctctattt  2101


Query: 1670  ggtgccatgaaaggaggaagcaaattcaaattaaaaactggaacagtagggaagttaccc  1729
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2102  ggtgccatgaaaggaggaagcaaattcaaattaaaaactggaacagtagggaagttaccc  2161


Query: 1730  cccaagcgtccagaactccctccaactctaa  1760
             |||||||||||||||||||||||||||||||
Sbjct: 2162  cccaagcgtccagaactccctccaactctaa  2192

 Score = 1287 bits (649), Expect = 0.0
 Identities = 693/701 (98%), Gaps = 5/701 (0%)
 Strand = Plus / Plus


Query: 1     gttgaggatggctgacattctctctcagtcagagaccctggcgtcgcaagacctcagtgg  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 437   gttgaggatggctgacattctctctcagtcagagaccctggcgtcgcaagacctcagtgg  496


Query: 61    ggacttcaagaagccagctctgccggtgtccccagcggcgcggagtaaggccccggccag  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 497   ggacttcaagaagccagctctgccggtgtccccagcggcgcggagtaaggccccggccag  556


Query: 121   cagttcttcaaaccctgaggaggtacagaaggaagggcccactgcgttgcaggactccaa  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 557   cagttcttcaaaccctgaggaggtacagaaggaagggcccactgcgttgcaggactccaa  616


Query: 181   ttctggggagcccgacatccctcctcctcagccggactgcggtgattttaggagtctaca  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 617   ttctggggagcccgacatccctcctcctcagccggactgcggtgattttaggagtctaca  676


Query: 241   ggaggagcagtcgcgcccacgacagcggtttcttcccctggcggtccagcccgggctcc  300
             |||||||||||||||||||| ||||||||||||||||||||||||||||||| |||||||||
Sbjct: 677   ggaggagcagtcgcgcccccgacagcggtttcttcccctggcggtccag-ccgggctcc  735


Query: 301   cccctaccaagagcctccatggggtggccctgccacagcccccctacagcttagagaccct  360
             |||||||||||||||||||||||||||| | |||||||||||||||||||||||||||| |||
Sbjct: 736   cccctaccaagagcctccatggggtgccgctgccacagcccccctacagcttagaga-cct  794
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Query: 361   gaagggcggcactatccttggcacccgtagcttgaaagggacgagttactgccttttcgg  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 795   gaagggcggcactatccttggcacccgtagcttgaaagggacgagttactgccttttcgg  854


Query: 421   gaggctgtctggctgcgacgtgtgcctggagcacc-cttcggtgtctcggtaccacgcag  479
             |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct: 855   gaggctgtctggctgcgacgtgtgcctggagcaccacttcggtgtctcggtaccacgcag  914


Query: 480   tgctgcagcacagggcgtccggccctgacggagaatgcgacagcaacgggccgggcttct  539
             |||||||||||| ||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct: 915   tgctgcagcaca-ggcgtccgg-cctgacggagaatgcgacagcaacgggccgggcttct  972


Query: 540   acctctacgatctgggaagcacccatggcacttttctcaacaaaactcgcatcccacctc  599
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 973   acctctacgatctgggaagcacccatggcacttttctcaacaaaactcgcatcccacctc  1032


Query: 600   gcacctactgtcgagtccacgttgggcatgttgttcgctttggaggcagcacccggctct  659
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1033  gcacctactgtcgagtccacgttgggcatgttgttcgctttggaggcagcacccggctct  1092


Query: 660   ttatcctgcagggaccagaggaagaccgagaggcagaatcc  700
             |||||||||||||||||||||||||||||||||||||||||
Sbjct: 1093  ttatcctgcagggaccagaggaagaccgagaggcagaatcc  1133

 Score =  222 bits (112), Expect = 8e-55
 Identities = 112/112 (100%)
 Strand = Plus / Plus


Query: 1850  ctggaggatggaagcctcagtaggccacagccagagatagagccagaagcagcagtgcag  1909
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2282  ctggaggatggaagcctcagtaggccacagccagagatagagccagaagcagcagtgcag  2341


Query: 1910  gaaatgaggcctcccacagatctcacacattttaaagaaacccaaacccatg  1961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2342  gaaatgaggcctcccacagatctcacacattttaaagaaacccaaacccatg  2393

>gi|2661089|gb|AF035526.1|AF035526 Mus musculus kanadaptin mRNA, complete cds
          Length = 2344

 Score = 1340 bits (676), Expect = 0.0
 Identities = 1085/1222 (88%)
 Strand = Plus / Plus


Query: 532   gggcttctacctctacgatctgggaagcacccatggcacttttctcaacaaaactcgcat  591
             ||||||| || |||||||||||||||||| ||||| ||||| || |||||||||||||||
Sbjct: 435   gggcttttatctctacgatctgggaagtacccacggcacgttcctcaacaaaactcgcat  494


Query: 592   cccacctcgcacctactgtcgagtccacgttgggcatgttgttcgctttggaggcagcac  651
             ||||||| ||||| |||||| |||||||||| ||||||||   | |||||||||||||||
Sbjct: 495   cccaccccgcacttactgtagagtccacgtcgggcatgtaatgcgctttggaggcagcac  554


Query: 652   ccggctctttatcctgcagggaccagaggaagaccgagaggcagaatccgagttaacagt  711
             ||||||||||||||||| ||||||||||||||||||||||||||||||| || ||||||||
Sbjct: 555   tcggctctttatccttcagggaccagaggaagaccgagaggcagaatctgaattaacagt  614
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Query: 712   aacacagttgaaggaattgcgcaagcagcagcaaatattgttggrgaagaagatgctagg  771
             |||||||||||||||||||||||| || |||||||| ||||| |||| |||||||||| ||||
Sbjct: 615   aacacagttgaaggaattgcgtaaacagcagcagatattattggagaagaagatgttagg  674


Query: 772   agaagactcagatgaagaagaggaaatggatacctctgaaaggaagataaatgctggtag  831
             |||||||||||||||||||||| |||      ||||| |||||| |||||| | |    || |
Sbjct: 675   tgaagactcagatgaagaagaagaagcaaataccactgaagggaagagcagtagaagtgg  734


Query: 832   ccaagatgatgagatgggttgcacctggggaatgggagaagatgcagtagaggatgatgc  891
             ||||||||||| |||| ||||| |||||||||||||||||||||||| || |||||||| ||
Sbjct: 735   tcaagatgatgagctgggctgcacgtggggaatgggagaagatgctgtggaggatgaagc  794


Query: 892   tgaagagaaccctattgtcttagagtttcagcaggaaagggaggcctttttatataaagga  951
             ||||||||||||| |||| ||||||| |||||||||| |||| || |||||||||||||||
Sbjct: 795   tgaagagaacccccattgccttagattttcagcaggaccgggaagcgtttttatataaagga  854


Query: 952   tcccaaaaaggctctccaaggcttttttgaccgagaaggagaagaattagaatatgaatt  1011
             ||| || ||||||||| ||||||||| ||||||||||||||||||||||| |||||||||||
Sbjct: 855   tccaaagaaggctcttcaaggcttctttgaccgagaaggagaagagttagaatatgaatt  914


Query: 1012  tgatgaacagggacatagcacttggctctgcagggtgagattacctgtggacgattcaac  1071
             |||||| || ||||| ||||||||||||||||||||||||||| ||||||| || |||||||||
Sbjct: 915   tgatgagcaaggacacagcacttggctctgcagggtgaggttacctgtagatgattcaac  974


Query: 1072  tggaaaacaactggtggctgaggccattcactcaggaaagaaaaaagaagcaatgatcca  1131
             ||| ||||| |||||||||||||||||||||||||||||||||||||||| |||||||| | ||
Sbjct: 975   tgggaaacagctggtggctgaggccattcactcaggaaagaaaaaggaagcaatggtaca  1034


Query: 1132  gtgctcattggaagcttgtcggattcttgacactttgggattgcttcggcaggaagcagt  1191
             ||||||  ||||||| || ||| | ||||| || |||| ||||| ||||||||||||||||
Sbjct: 1035  gtgctcgctggaagcctgccgggtccttgatacactgggcttgctacggcaggaagcagt  1094


Query: 1192  atctcggaaaaggaaagccaagaactgggaagatgaagactttttatgatagtgatgatga  1251
             |||||||||||||||||||||||||||||||||||||||| || ||||||||||||||| |||||
Sbjct: 1095  atctcggaaaaggaaagccaagaactgggaagatgaggattttttatgatagtgacgatga  1154


Query: 1252  cacatttcttgataggactggcctgattgagaagaagcgtctgaacagaatgaagaaggc  1311
             |||||  || ||| |||||||||||| | ||||||||||| ||||||| | |||||||||||
Sbjct: 1155  tacattcctcgatcggactggcctggtagagaagaagcgcctgaaccggatgaagaaggc  1214


Query: 1312  tggcaagattgatgagaagccagagacctttgaatcattggttgcaaaattaaatgatgc  1371
             |||  ||| ||||||||||||||||| || ||||| ||| |||||||||| ||||||||||
Sbjct: 1215  tgggaagcttgatgagaagccagaaacttttgagtcactggttgcaaagttaaatgatgc  1274


Query: 1372  tgaaagggaactttctgaaatttctgagagattgaaagcctcaagccaagttctatcaga  1431
             |||||||||||| | |||||||||||| || | || || |||||| ||||||| |||||
Sbjct: 1275  cgaaagggaactcgccgaaatttctgaaaggctcaaggcttcaagcaaagttctgtcaga  1334


Query: 1432  gtctccatctcaggattctttagatgcgttcatgtcagaaatgaaatcaggcagtacatt  1491
             | |  |||||||||| |||||||||||| ||||||||||||||||||||||||||| |||||
Sbjct: 1335  gccatcatctcaggactctttagatgcattcatgtcagaaatgaaatcaggcagcacatt  1394
```

```
Query: 1492  agatggtgtgtcccggaagaaacttcacctgagaactttttgaactgaggaaagaacaaca  1551
             ||||||| |||||||||||||||||||||||||||||| |||||||||||| || |||||||||||||
Sbjct: 1395  agatggggtgtcccggaagaaacttcacctgaggactttttgaactaagaaaagaacaaca  1454


Query: 1552  gagacttaaagggttaataaaaattgtaaagccagcagagattccagaactaaaaaagac  1611
             | ||||||||||||||||||||| ||||||||||| ||||||||| |||||||||||||||||
Sbjct: 1455  gcgacttaaagggttaataaaacttgtaaagccggcagagatcccagaactaaaaaagac  1514


Query: 1612  tgaaactcagactacaggtgcagaaaacaaagctaaaaagcttacattgcctctatttgg  1671
             ||||    |||||||||| |||||||||||||| |||| || ||| ||||||||||| ||||||
Sbjct: 1515  tgaacttcagactacaaatgcagaaaacaaaactaagaaacttgcattgcctctctttgg  1574


Query: 1672  tgccatgaaaggaggaagcaaattcaaattaaaaactggaacagtagggaagttacccccc  1731
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||| || ||
Sbjct: 1575  tgccatgaaaggaggaagcaaattcaaattaaaaactgggacagtagggaagttgccacc  1634


Query: 1732  caagcgtccagaactccctcca  1753
             ||||||||||||||||||||||||
Sbjct: 1635  caagcgtccagaactccctcca  1656


 Score = 87.7 bits (44), Expect = 3e-14
 Identities = 122/148 (82%)
 Strand = Plus / Plus


Query: 327  gccctgccacagcccccctacagcttagagaccctgaagggcggcactatccttggcaccc  386
            |||| |||||| |||||||||||||||   | || |||||||||| ||||| |||||||||||||
Sbjct: 230  gcccagccacggccccctacagtctcgaaaccctgaagggtggcaccatccttggcaccc  289


Query: 387  gtagcttgaaagggacgagttactgccttttcgggaggctgtctggctgcgacgtgtgcc  446
            | | |||||||||  ||||| | |||| |||||||||| ||  || | || ||| | || |
Sbjct: 290  gcaccttgaaagacacgagctgctgcttttcgggagacttgctagttgtgacatatgtc  349


Query: 447  tggagcacccttcggtgtctcggtacca  474
            ||||||| |||||| |||||||||||||||
Sbjct: 350  tggagcatccttccgtgtctcggtacca  377


>gi|1029496|emb|Z58265.1|HS33F3R H.sapiens CpG island DNA genomic Mse1 fragment, clone 33f3, r
           read cpg33f3.rt1f
           Length = 290

 Score =  428 bits (216), Expect = e-117
 Identities = 226/230 (98%)
 Strand = Plus / Minus


Query: 442  gtgcctggagcacccttcggtgtctcggtaccacgcagtgctgcagcacagggcgtccgg  501
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct: 290  gtgcctggagcacccttcggtgtctcggtaccacgcagtgctgcagcacagggcgtctgg  231


Query: 502  ccctgacggagaatgcgacagcaacgggccgggcttctacctctacgatctgggaagcac  561
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 230  ccctgacggagaatgcgacagcaacgggccgggcttctacctctacgatctgggaagcac  171


Query: 562  ccatggcactttttctcaacaaaactcgcatcccacctcgcacctactgtcgagtccacgt  621
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
```

```
Sbjct: 170  ccatggcacttttctcaacaaaactcgcatcccacctcgcacctactgtcgagnccacgt 111


Query: 622  tgggcatgttgttcgctttggaggcagcacccggctctttatcctgcagg 671
            |||||||||||||||||||||||||||| ||||||||||| |||||||||||||||||||
Sbjct: 110  tgggcatgttgttcgctttggagacagcacccgnctctttatcctgcagg 61

>gi|11182219|emb|AL357559.16|AL357559 Human DNA sequence from clone RP11-393M18 on chromosome
            sequence [Homo sapiens]
         Length = 190912

 Score =  141 bits (71), Expect = 2e-30
 Identities = 144/167 (86%), Gaps = 1/167 (0%)
 Strand = Plus / Plus


Query: 1551    agagacttaaagggttaataaaaattgtaaagccagcagagattccagaactaaaaaaga 1610
               |||||||||||| || |||||||||||||||||||||||||||   |||||||||| | ||
Sbjct: 189905  agagacttaaaggattgataaaaattgtaaagccagcagagacctcagaactaaacatga 189964


Query: 1611    ctgaaactcagactacaggtgcagaaaacaaagctaaaaagcttacattgcctctatttg 1670
                |||||  | |||||| || |||| |   | |||||||| ||||||||| |||| |||| || |
Sbjct: 189965  ttgaaaattagactaaagatgcacacga-aaagctacaaagcttatattgactctcttgg 190023


Query: 1671    gtgccatgaaaggaggaagcaaattcaaattaaaaactggaacagta 1717
               ||||||| |||||||||||||||||| |||||||||||||||||||||
Sbjct: 190024  gtgccataaaaggaggaagcaaattgaaattaaaaactggaacagta 190070

 Score = 91.7 bits (46), Expect = 2e-15
 Identities = 64/70 (91%)
 Strand = Plus / Plus


Query: 1307    aaggctggcaagattgatgagaagccagagacctttgaatcattggttgcaaaattaaat 1366
               |||||||| ||||||||||||||||| ||||||||||| || | ||||||||||| ||||||
Sbjct: 189691  aaggctgggaagattgatgagaaggcagagacctttgcattactggttgcaaagttaaat 189750


Query: 1367    gatgctgaaa 1376
               ||||||||||
Sbjct: 189751  gatgctgaaa 189760

 Score = 87.7 bits (44), Expect = 3e-14
 Identities = 65/72 (90%)
 Strand = Plus / Plus


Query: 1407    aagcctcaagccaagttctatcagagtctccatctcaggattctttagatgcgttcatgt 1466
               |||||||||||| ||||||||||||| || | ||||||||| |||||||||||| ||||||||
Sbjct: 189765  aagcctcaagcaaagttctatcagaatcacaatctcaggcttctttagatgtgttcatgt 189824


Query: 1467    cagaaatgaaat 1478
               ||||| ||||||
Sbjct: 189825  cagaagtgaaat 189836

 Score = 73.9 bits (37), Expect = 5e-10
 Identities = 40/41 (97%)
 Strand = Plus / Plus


Query: 1213    gaactgggaagatgaagactttatgatagtgatgatgaca 1253
               ||||||||||||||||||||||||||||| ||||||||||||
```

```
Sbjct: 189600 gaactgggaagatgaagacttttatgagagtgatgatgaca 189640


 Score = 56.0 bits (28), Expect = 1e-04
 Identities = 28/28 (100%)
 Strand = Plus / Plus



Query: 996    aattagaatatgaatttgatgaacaggg 1023
              ||||||||||||||||||||||||||||
Sbjct: 189384 aattagaatatgaatttgatgaacaggg 189411


 Score = 44.1 bits (22), Expect = 0.44
 Identities = 58/70 (82%)
 Strand = Plus / Plus



Query: 658    ctttatcctgcagggaccagaggaagaccgagaggcagaatccgagttaacagtaacaca 717
              |||| ||||||| ||||||||| ||||||| || || | ||||||| ||| |||||||   ||
Sbjct: 189057 ctttgtcctgcaaggaccagaagaagactgaaagactgaatccaagtgaacagtagtgca 189116



Query: 718    gttgaaggaa 727
              ||||||||||
Sbjct: 189117 gttgaaggaa 189126


 Score = 40.2 bits (20), Expect = 6.9
 Identities = 60/72 (83%), Gaps = 1/72 (1%)
 Strand = Plus / Plus



Query: 1064   gattcaactggaaaacaactggtggctgaggccattcactcaggaaagaaaaaa-gaagc 1122
              |||||| |||||||||||||      ||||||| |||||| |||| |||| ||||||||| ||| |
Sbjct: 189447 gattcatctggaaaacaacgccaggctgaagccatgcacttaggagagaaaaaaggaaac 189506



Query: 1123   aatgatccagtg 1134
              || |||||||||
Sbjct: 189507 aaagatccagtg 189518

>gi|11181843|gb|AC017028.11|AC017028 Homo sapiens BAC clone RP11-275G7 from 2, complete sequen
          Length = 201971

 Score = 48.1 bits (24), Expect = 0.028
 Identities = 27/28 (96%)
 Strand = Plus / Minus



Query: 1968   tctttcttctccttcctgtgttgttcag 1995
              ||||||||||| |||||||||||||||||
Sbjct: 172682 tctttcttcttcttcctgtgttgttcag 172655

>gi|14010785|gb|AC069543.4|AC069543 Homo sapiens chromosome 10 clone RP11-393H5, complete sequ
          Length = 179787

 Score = 46.1 bits (23), Expect = 0.11
 Identities = 23/23 (100%)
 Strand = Plus / Plus



Query: 984    gagaaggagaagaattagaatat 1006
              |||||||||||||||||||||||
Sbjct: 127574 gagaaggagaagaattagaatat 127596

>gi|10443437|emb|AL356421.10|AL356421 Human DNA sequence from clone RP11-550C4 on chromosome 6
          sequence [Homo sapiens]
```

```
        Length = 170532

 Score = 46.1 bits (23), Expect = 0.11
 Identities = 23/23 (100%)
 Strand = Plus / Minus


Query: 1680   aaggaggaagcaaattcaaatta 1702
              |||||||||||||||||||||||
Sbjct: 92560 aaggaggaagcaaattcaaatta 92538

   Database: nt
     Posted date:  May 11, 2001  4:10 AM
   Number of letters in database: -1,072,656,299
   Number of sequences in database:  858,416

Lambda       K        H
    1.37     0.711     1.31

Gapped
Lambda       K        H
    1.37     0.711     1.31


Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 6729269
Number of Sequences: 858416
Number of extensions: 6729269
Number of successful extensions: 48683
Number of sequences better than 10.0: 87
length of query: 2644
length of database: 3,222,310,993
effective HSP length: 22
effective length of query: 2622
effective length of database: 3,203,425,841
effective search space: 8399382555102
effective search space used: 8399382555102
T: 0
A: 30
X1: 6 (11.9 bits)
X2: 15 (29.7 bits)
S1: 12 (24.3 bits)
S2: 20 (40.2 bits)
```